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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/898,234

DATE: 08/28/2001
TIME: 11:57:30

Input Set : A:\98385\seq.txt
Output Set: N:\CRF3\08282001\I898234.raw

3 <110> APPLICANT: Hauptmann, Rudolph
4 Himmller, Adolph
5 Maurer-Fogy, Ingrid
6 Stratowa, Christian
8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
9 Them
11 <130> FILE REFERENCE: 98,385-I
14 <140> CURRENT APPLICATION NUMBER: 09/898,234
15 <141> CURRENT FILING DATE: 2001-07-03
17 <150> PRIOR APPLICATION NUMBER: 09/525,998
18 <151> PRIOR FILING DATE: 2000-03-15
20 <150> PRIOR APPLICATION NUMBER: 08/383,676
21 <151> PRIOR FILING DATE: 1995-02-01
23 <150> PRIOR APPLICATION NUMBER: 08/153,287
24 <151> PRIOR FILING DATE: 1993-11-17
26 <150> PRIOR APPLICATION NUMBER: 07/821,750
27 <151> PRIOR FILING DATE: 1992-01-02
29 <150> PRIOR APPLICATION NUMBER: 07/511,430
30 <151> PRIOR FILING DATE: 1990-04-20
32 <160> NUMBER OF SEQ ID NOS: 87
34 <170> SOFTWARE: PatentIn Ver. 2.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 1368
38 <212> TYPE: DNA
39 <213> ORGANISM: Homo sapiens
41 <220> FEATURE:
42 <221> NAME/KEY: CDS
43 <222> LOCATION: (1)..(1368)
45 <220> FEATURE:
46 <221> NAME/KEY: sig_peptide
47 <222> LOCATION: (1)..(87)
49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (88)..(120)
52 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
53 extracellular proteases following secretion.
55 <220> FEATURE:
56 <221> NAME/KEY: misc_feature
57 <222> LOCATION: (606)..(633)
58 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
59 extracellular proteases following secretion.
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62 atg ggc ctc tcc acc gtg cct gac ctg ctg cca ctg gtg ctc ctg 48
63 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Pro Leu Val Leu Leu
64 1 5 10 15
66 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96
67 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro

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P. 5

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Input Set : A:\98385Iseq.txt
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68	20	25	30	
70	cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa			144
71	His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys			
72	35	40	45	
74	tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa			192
75	Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys			
76	50	55	60	
78	gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac			240
79	Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp			
80	65	70	75	80
82	tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc			288
83	Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu			
84	85	90	95	
86	aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg			336
87	Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val			
88	100	105	110	
90	gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg			384
91	Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg			
92	115	120	125	
94	aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc			432
95	Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe			
96	130	135	140	
98	aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag			480
99	Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu			
100	145	150	155	160
102	aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa			528
103	Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu			
104	165	170	175	
106	aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg			576
107	Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr			
108	180	185	190	
110	aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca			624
111	Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser			
112	195	200	205	
114	ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt			672
115	Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu			
116	210	215	220	
118	tta tcc ctc ctc att ggt tta atg tat cgc tac caa cgg tgg aag			720
119	Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys			
120	225	230	235	240
122	tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag			768
123	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
124	245	250	255	
126	ggg gag ctt gaa gga act act aag ccc ctg gcc cca aac cca agc			816
127	Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
128	260	265	270	
130	ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg			864
131	Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
132	275	280	285	

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Input Set : A:\98385Iseq.txt
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134	ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt	912
135	Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys	
136	290 295 300	
138	ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg	960
139	Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly	
140	305 310 315 320	
142	gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac	1008
143	Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn	
144	325 330 335	
146	ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac	1056
147	Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp	
148	340 345 350	
150	act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg	1104
151	Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro	
152	355 360 365	
154	ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag	1152
155	Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu	
156	370 375 380	
158	atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa	1200
159	Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln	
160	385 390 395 400	
162	tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc	1248
163	Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala	
164	405 410 415	
166	acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc	1296
167	Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly	
168	420 425 430	
170	tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg	1344
171	Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro	
172	435 440 445	
174	ccc gcg ccc agt ctt ctc aga tga	1368
175	Pro Ala Pro Ser Leu Leu Arg	
176	450 455	
179	<210> SEQ ID NO: 2	
180	<211> LENGTH: 455	
181	<212> TYPE: PRT	
182	<213> ORGANISM: Homo sapiens	
184	<400> SEQUENCE: 2	
185	Met Gly Leu Ser Thr Val Pro Asp Leu Leu Pro Leu Val Leu Leu	
186	1 5 10 15	
188	Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro	
189	20 25 30	
191	His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys	
192	35 40 45	
194	Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys	
195	50 55 60	
197	Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp	
198	65 70 75 80	
200	Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu	

RAW SEQUENCE LISTING
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Input Set : A:\98385Iseq.txt
Output Set: N:\CRF3\08282001\I898234.raw

201	85	90	95
203	Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val		
204	100	105	110
206	Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg		
207	115	120	125
209	Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe		
210	130	135	140
212	Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu		
213	145	150	155
215	Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu		
216	165	170	175
218	Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr		
219	180	185	190
221	Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser		
222	195	200	205
224	Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu		
225	210	215	220
227	Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys		
228	225	230	235
230	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu		
231	245	250	255
233	Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser		
234	260	265	270
236	Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val		
237	275	280	285
239	Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys		
240	290	295	300
242	Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly		
243	305	310	315
245	Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn		
246	325	330	335
248	Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp		
249	340	345	350
251	Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro		
252	355	360	365
254	Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu		
255	370	375	380
257	Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln		
258	385	390	395
260	400		
261	Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala		
263	405	410	415
264	420	425	430
266	435	440	445
269	Pro Ala Pro Ser Leu Leu Arg		
270	450	455	
273	<210> SEQ ID NO: 3		
274	<211> LENGTH: 483		

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/898,234

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Input Set : A:\98385Iseq.txt
Output Set: N:\CRF3\08282001\I898234.raw

275 <212> TYPE: DNA
 276 <213> ORGANISM: Homo sapiens
 278 <220> FEATURE:
 279 <221> NAME/KEY: CDS
 280 <222> LOCATION: (1)..(483)
 282 <400> SEQUENCE: 3
 283 gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat tcg 48
 284 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
 285 1 5 10 15
 287 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt 96
 288 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
 289 20 25 30
 291 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144
 292 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
 293 35 40 45
 295 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 192
 296 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
 297 50 55 60
 299 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 240
 300 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
 301 65 70 75 80
 303 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 288
 304 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
 305 85 90 95
 307 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg 336
 308 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
 309 100 105 110
 311 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc 384
 312 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
 313 115 120 125
 315 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432
 316 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
 317 130 135 140
 319 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480
 320 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
 321 145 150 155 160
 323 aat
 324 Asn
 327 <210> SEQ ID NO: 4
 328 <211> LENGTH: 161
 329 <212> TYPE: PRT
 330 <213> ORGANISM: Homo sapiens
 332 <400> SEQUENCE: 4
 333 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
 334 1 5 10 15
 336 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
 337 20 25 30
 339 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
 340 35 40 45

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/898,234

DATE: 08/28/2001
TIME: 11:57:31

Input Set : A:\98385Iseq.txt
Output Set: N:\CRF3\08282001\I898234.raw

L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36